

uence Range: 1 to 5578

AATCATACTGAGCTTGGCAAATTCAATCTGAGCGCAAAAGCATCTTCAGGAGCGAGAAAAGGCCCAAAATAATGTGAG ATGCATTTGAC GTC CGA ATCGT GCT GCC TTCG CTC

230	240	250	260	270	280	290	300	310																			
*	*	*	*	*	*	*	*	*																			
CTG	GTC	TTT	ATA	GCG	CCT	GCA	TGT	GGG	TAT	ATG	ACC	GCC	ATC	CCA	CGA	CTA	CCA	CCG	GAT	AAT	TTC	CCA	Leu				
Leu	Val	Phe	Ile	Ala	Pro	Ala	Val	Glu	Arg	Cys	Gly	Tyr	Met	Thr	Ala	Ile	Pro	Arg	Leu	Pro	Asn	Asp	Asn	Leu			
320	330	340	350	360	370	380	390	400																			
*	*	*	*	*	*	*	*	*																			
GTA	CTA	AAT	TTT	GAA	GGC	CAG	ACA	TGG	AGT	CAG	CCC	CTG	CTC	CCC	CCG	GAG	CGG	GAT	GAC	CTG	TGC	ATG	GAC	GCC	TAC	CAC	GTG
Val	Leu	Asn	Phe	Glu	Gly	Gln	Thr	Tyr	Ser	Gln	Arg	Pro	Leu	Pro	Leu	Pro	Glu	Arg	Asn	Asp	Leu	Cys	Met	Asn	Asp	Leu	Val

500 * 510 * 520 * 530 * 540 * 550 * 560 * 570 * 580 *

CAT CAT CAC GCA AGA CAG CAT TAC GAG TTG CCC CGC ATG CAG CAG TAC ATG TTC AAT GTG CGC GTG GAC GGC CAG TCG CTC GTG GCA CGC
His His Ala Arg Gln His Tyr Glu Leu Pro Gly Met Gln Gln Tyr Met Phe Asn Val Arg Val Asp Gly Gln Ser Leu Val Ala Gly>

770	780	790	800	810	820	830	840	850																
*	*	*	*	*	*	*	*	*																
TTG	ACA	GAA	TGC	ACA	TAC	CAA	GTA	TCG	GAC	GCG	GAC	CGG	ATC	AGC	ACA	GAG	TTC	AGG	ATC	GAC	AGC	GTT	GGC	GAC

* GGC GCG ACC TGG TAC ATC CAA AAC CCC AAT ATC CCG AGG CAA GAA CGG TGG ATG TGG CTA AAT ACC ATA CGG GGT AAA ACC TGG CTC AAC TGC * 940

the only way to do this is to use the `File` menu.

Fig. 1.

1040	1050	1060	1070	1080	1090	1100	1110	1120
*	*	*	*	*	*	*	*	*
GTC AAC AGT CCG CTG CAT ATA TTC AGC GTC ACA GCC GAC GCT GCA CAC ACC CAC GTC ACT ATG GTG CAA GTG CCA GCG AAC								
Val Thr Ser Pro Leu His Ile Phe Ser Val Thr Val His Thr Val Met Val Thr Val Met Val Ala Asn >								
1130	1140	1150	1160	1170	1180	1190	1200	1210
*	*	*	*	*	*	*	*	*
GAC GGA GAC ACT GAG ATC AAT ATG CCT ATC AAC TAC AGG CTG ATC ACA AAT GAG GAA GAC ACA TTC TTC AGC ATT GAG GCC CTG CCT GCT								
Asp Gly Asp Thr Glu Ile Asn Met Pro Ile Asn Tyr Arg Leu Ile Asn Asp Thr Phe Ser Ile Glu Ala Leu Pro Gly >								
1220	1230	1240	1250	1260	1270	1280	1290	1300
*	*	*	*	*	*	*	*	*
GGA AAA AGC GGG GCT GTA TTC CTC GTG TCG CCA ATT GAC CGC GAC ACA CTG CAA CGA GAG GTG TTT CCA CTT ACG ATC GTC GCT TAC AAA								
Gly Lys Ser Gly Ala Val Ser Pro Ile Asp Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr Ile Val Ala Tyr Lys >								
1310	1320	1330	1340	1350	1360	1370	1380	1390
*	*	*	*	*	*	*	*	*
TAT GAT GAG GAG GCC TTC TCC ACA TCA AAC GTG GTC ATC ATT GTG ACA GAC ATC AAC GAC CAA ACA CCT GAA CCT ATA CAC AAG GAA								
Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val Ile Val Asn Asp Ile Asn Asp Gln Arg Pro Glu Pro Ile His Lys Glu >								
1400	1410	1420	1430	1440	1450	1460	1470	1480
*	*	*	*	*	*	*	*	*
TAT CGA CTG GCA ATC ATG GAG GAG CCC CTG ACC CTC AAC TTC GAT AAA GAA TTC GGA TTT CAT GAT AAG GAT TTA GGT CAA AAC GCT								
Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr Leu Asn Phe Asp Lys Glu Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala >								
1490	1500	1510	1520	1530	1540	1550	1560	1570
*	*	*	*	*	*	*	*	*
CAG TAC ACG GTG CGT CTA GAG AGC GAC CCT CCA GGC GCT GCT GAG GCA TTC TAC ATA GCG CCT GAA GTC GGC TAC CAG CGA CAG ACC								
Gln Tyr Thr Val Ile Met Gly Thr Leu Asn His Ser Met Leu Asp Pro Pro Gly Ala Ala Glu Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln Thr >								
1580	1590	1600	1610	1620	1630	1640	1650	1660
*	*	*	*	*	*	*	*	*
TTC ATC ATG GGC ACC CTC AAT CAC TCC ATG CTG GAT TAC GAA GTG CCA GAG TTT CAG AGT ATT ACG ATT CGG GTG GTA GCG ACC GAC AAC								
Phe Ile Met Gly Thr Val Ile Asn His Ser Val Ala Asp Trp Asn Ile Asn Trp Asn Ile Asp Leu Ile Asp His Ile Leu Val His Ile Val Gln Asn >								
1670	1680	1690	1700	1710	1720	1730	1740	1750
*	*	*	*	*	*	*	*	*
AAC GAC AGC AGG CAC GTG GGC GTC GCG TTG GTC ATT GAC CTC ATC AAT TGG AAC GAT GAG CAG CCG ATC TTC GAA CAC GCC GTG CAG								
Asn Asp Thr Arg His Val Gly Val Ala Val Asn Asp Ile Asn Asp Ile Asn Trp Asn Ile Asp Leu Ile Asp His Ile Leu Val His Ile Val Gln >								
1760	1770	1780	1790	1800	1810	1820	1830	1840
*	*	*	*	*	*	*	*	*
ACC GTC ACC TTC GAC GAG ACT GAA GGC GAG GGG TTC TTC GTC GCC AAG GCG GTT GCA CAC GAC AGA GAC ATC GGG GAT GTC GTC GAC CAT								
Thr Val Thr Phe Asp Glu Thr Glu Gly Glu Gly Phe Val Ala Lys Ala Val Ala His Asp Arg Asp Ile Gly Asp Val Val Glu His Ile Val His >								
1850	1860	1870	1880	1890	1900	1910	1920	1930
*	*	*	*	*	*	*	*	*
ACT TTA TTG GGT AAC GCT GTC ACC ATC GAC AAA CTC ACC GGC GAC ATC CGC GTC TCA GCT AAC GAC TCC TTC AAC TAC CAT								
Thr Leu Leu Gly Ala Val Asn Phe Leu Thr Ile Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp Ser Phe Asn Tyr His >								
1940	1950	1960	1970	1980	1990	2000	2010	2020

Fig / 60-1X)

GCT	ACA	GAC	CAG	GGG	ACG	CCA	GGA	CGG	CCG	GAC	CCC	ACG	CAA	GGA	CCT	AGA	TTC		
Ala	Thr	Asp	Gln	Gly	Thr	Asp	Pro	Gly	Thr	Asp	Pro	Gly	Thr	Asp	Pro	Gly	Pro	Phe	
3920	3930	*	*	*	*	3940	*	*	*	3950	3960	*	*	*	3970	3980	3990	4000	
GGC	TCC	TCA	GAA	CAT	GCT	GTC	GCT	GCC	GCC	AAG	AGT	GCC	ATG	GAA	GAG	TCT	CAC	CAC	
Ala	Ser	Ser	Glu	His	Ala	Val	Ala	Leu	Ile	Glu	Lys	Ser	Ala	Gly	Met	Glu	Glu	Ser	His
4010	4020	*	*	*	*	4030	*	*	*	4040	4050	*	*	*	4060	4070	4080	4090	
CAT	CTC	TGT	GAA	GAC	GAC	TGT	CAC	AGC	ATT	TAC	TAT	CGT	ATT	ATC	GAT	TTC	GGC	CTG	
His	Leu	Cys	Glu	Asp	Cys	His	Ser	Ile	Tyr	Tyr	Tyr	Arg	Ile	Asp	Gly	Asn	Ser	Glu	Gly
4100	4110	*	*	*	*	4120	*	*	*	4130	4140	*	*	*	4150	4160	4170	4180	
AGG	TTG	TTC	CTG	AAG	AAG	CTG	ATA	AGG	GAA	CAA	AGT	GCC	TCC	CAC	ACT	CTG	CAA	GTG	
Arg	Leu	Phe	Leu	Lys	lys	Glu	Leu	Ile	Arg	Glu	Gln	Ser	Ala	Ser	His	Thr	Leu	Gln	Val
4190	4200	*	*	*	*	4210	*	*	*	4220	4230	*	*	*	4240	4250	4260	4270	
CCA	CRT	CCT	GCT	TCC	ATC	CTT	ACT	GTC	ACT	GTT	ACC	GTC	AGG	GCA	GAC	CCT	CGT	CCA	
Pro	Leu	Pro	Ala	Ser	Ile	Ile	Leu	Thr	Val	Thr	Val	Thr	Val	Arg	Glu	Ala	Asp	Pro	Arg
4280	4290	*	*	*	*	4300	*	*	*	4310	4320	*	*	*	4330	4340	4350	4360	
ATA	TCC	ACA	GCG	GAC	TCC	ATC	CGG	AGA	GAG	CTG	CTC	AGA	TTA	CAT	GCG	ACC	CAG	TCT	
Ile	Ser	Thr	Ala	Asp	Ser	Ile	Gly	Arg	Glu	Leu	Leu	Arg	Leu	Arg	Leu	His	Ala	Thr	Gly
4370	4380	*	*	*	*	4390	*	*	*	4400	4410	*	*	*	4420	4430	4440	4450	
GAT	ACA	ATG	GTA	GTG	GAC	CCC	AGC	CTG	GCA	GAG	CTG	AGA	CAG	TGC	GCT	TTC	GTA	CTG	
Asp	Thr	Met	Val	Val	Asp	Ser	Leu	Glu	Ala	Val	Arg	Gln	Ser	Ala	Phe	Val	Leu	Asn	Thr
4460	4470	*	*	*	*	4480	*	*	*	4490	4500	*	*	*	4510	4520	4530	4540	
CAG	CCC	ACG	GCC	ACG	ATG	CAT	GGG	CTG	TTC	AAA	TTC	GAA	GTC	ACA	GCT	ACT	GAC	GGC	
Gln	Pro	Thr	Ala	Thr	Met	His	Gly	Leu	Pho	Lys	Pho	Glu	Val	Thr	Ala	Thr	Asp	Arg	Thr
4550	4560	*	*	*	*	4570	*	*	*	4580	4590	*	*	*	4600	4610	4620	4630	
TAC	GTC	GTA	TCC	TCG	OAG	AAC	CGC	GTC	TAC	TTC	GTG	TTC	GTC	AAC	ACG	CTG	CAG	GTC	
Tyr	Val	Val	Ser	Ser	Gln	Asn	Arg	Val	Tyr	Pho	Val	Leu	Gln	Asn	Thr	Leu	Glu	Asp	Asp
4640	4650	*	*	*	*	4660	*	*	*	4670	4680	*	*	*	4690	4700	4710	4720	
TTC	AGC	GCT	GGG	TTC	AAC	ATC	GAC	CAA	GTG	GTG	CCC	GCT	AAC	GAC	CCC	GTC	ACC	GGC	
Phe	Ser	Ala	Gly	Phe	Asn	Met	Thr	Cys	Asn	Ile	Asp	Gln	Val	Val	Pro	Ala	Asn	Asp	Pro
4730	4740	*	*	*	*	4750	*	*	*	4760	4770	*	*	*	4780	4790	4800	4810	
CAG	ATG	GCG	GCC	ACT	TCA	TAC	GGG	ACA	ACG	TAC	CCG	TAC	TCG	ATG	AGA	TAG	A	ACAGATCCCTAGTCACCTAGTCCTGAGCTCGATAACAAACCC	
Gln	Met	Ala	Ala	Ala	Thr	Ser	Tyr	Thr	Gly	Thr	Tyr	Pro	Tyr	Ser	Leu	Met	Arg	***	xxx>
4840	4850	*	*	*	*	4860	*	*	*	4870	4880	*	*	*	4890	4900	4910	4920	
																		4940	
																		4950	

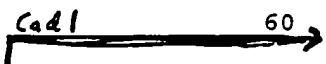
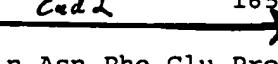
Figs. 1 (c), 7, X

KAY DEEVAL STAFFER:

ଶ୍ରୀମଦ୍ଭଗବତ:

Two et changes:

41	2105-08	'G' addition
	2627-8	deletion
	2668	'C' addition
	2678	'G' addition
	2946	rearrangement
	3464	rearrangement
	3471	deletion
	4935-6	addition
	4984-4892	addition
	4938	deletion
	5030	rearrangement
	5031	rearrangement
	5200	rearrangement
	5216	deletion
	5288	rearrangement
	5422	rearrangement

Met Ala Val Asp Val Arg Ile Ala Ala Phe Leu Leu Val Phe Ile Ala			
1	5	10	15
Pro Ala Val Leu Ala Gln Glu Arg Cys Gly Tyr Met Thr Ala Ile Pro			
20	25	30	
Arg Leu Pro Arg Pro Asp Asn Leu Pro Val Leu Asn Phe Glu Gly Gln			
35	40	45	
Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala Pro Glu Arg Asp Asp Leu			
50	55	<i>Cedl</i>	60
			
Cys Met Asp Ala Tyr His Val Ile Thr Ala Asn Leu Gly Thr Gln Val			
65	70	75	80
Ile Tyr Met Asp Glu Glu Ile Glu Asp Glu Ile Thr Ile Ala Ile Leu			
85	90	95	
Asn Tyr Asn Gly Pro Ser Thr Pro Phe Ile Glu Leu Pro Phe Leu Ser			
100	105	110	
Gly Ser Tyr Asn Leu Leu Met Pro Val Ile Arg Arg Val Asp Asn Gly			
115	120	125	
Ser Ala Ser His His His Ala Arg Gln His Tyr Glu Leu Pro Gly Met			
130	135	140	
Gln Gln Tyr Met Phe Asn Val Arg Val Asp Gly Gln Ser Leu Val Ala			
145	150	155	160
Gly Val Ser Leu Ala Ile Val Asn Ile Asp Asp Asn Ala Pro Ile Ile			
			
<i>Cedl</i>	165	170	175
Gln Asn Phe Glu Pro Cys Arg Val Pro Glu Leu Gly Glu Pro Gly Leu			
180	185	190	
Thr Glu Cys Thr Tyr Gln Val Ser Asp Ala Asp Gly Arg Ile Ser Thr			
195	200	205	
Glu Phe Met Thr Phe Arg Ile Asp Ser Val Arg Gly Asp Glu Glu Thr			
210	215	220	
Phe Tyr Ile Glu Arg Thr Asn Ile Pro Asn Gln Trp Met Trp Leu Asn			
225	230	235	240
Met Thr Ile Gly Val Asn Thr Ser Leu Asn Phe Val Thr Ser Pro Leu			
245	250	255	
His Ile Phe Ser Val Thr Ala Leu Asp Ser Leu Pro Asn Thr His Thr			
260	265	270	
Val Thr Met Met Val Gln Val Ala Asn Val Asn Ser Arg Pro Pro Arg			
275	280	285	

Cad 3

Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu Glu Lys Ser Tyr Gln
 290 295 300

Asn Phe Thr Val Arg Ala Ile Asp Gly Asp Thr Glu Ile Asn Met Pro
 305 310 315 320

Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser Ile
 325 330 335

Glu Ala Leu Pro Gly Gly Lys Ser Gly Ala Val Phe Leu Val Ser Pro
 340 345 350

Ile Asp Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr Ile Val
 355 360 365

Ala Tyr Lys Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val Val
 370 375 380

Cad 4

Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro Glu Pro Ile His Lys
 385 390 395 400

Glu Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr Leu Asn Phe
 405 410 415

Asp Lys Glu Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala Gln
 420 425 430

Tyr Thr Val Arg Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala
 435 440 445

Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln Thr Phe Ile Met
 450 455 460

Gly Thr Leu Asn His Ser Met Leu Asp Tyr Glu Val Pro Glu Phe Gln
 465 470 475 480

Ser Ile Thr Ile Arg Val Val Ala Thr Asp Asn Asn Asp Thr Arg His
485 485 490 495

Val Gly Val Ala Leu Val His Ile Asp Leu Ile Asn Trp Asn Asp Glu
 500 505 510

Gln Pro Ile Phe Glu His Ala Val Gln Thr Val Thr Phe Asp Glu Thr
 515 520 525

Glu Gly Glu Gly Phe Phe Val Ala Lys Ala Val Ala His Asp Arg Asp
 530 535 540

Ile Gly Asp Val Val Glu His Thr Leu Leu Gly Asn Ala Val Asn Phe
 545 550 555 560

Leu Thr Ile Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp
 565 570 575

Ser Phe Asn Tyr His Arg Glu Ser Glu Leu Phe Val Gln Val Arg Ala
580 585 590

Thr Asp Thr Leu Gly Glu Pro Phe His Thr Ala Thr Ser Gln Leu Val
595 600 605 cad 6

Ile Arg Leu Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu Pro
610 615 620

Arg Gly Ser Pro Gln Val Glu Glu Asn Val Pro Asp Gly His Val Ile
625 630 635 640

Thr Gln Glu Leu Arg Ala Thr Asp Pro Asp Thr Thr Ala Asp Leu Arg
645 650 655

Phe Glu Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly Arg Gln
660 665 670

Ala Asn Pro Asp Glu Phe Arg Asn Cys Val Glu Ile Glu Thr Ile Phe
675 680 685

Pro Glu Ile Asn Asn Arg Gly Leu Ala Ile Gly Arg Val Val Ala Arg
690 695 700

Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu Phe Glu Val Leu
705 710 715 720

Ser Leu Thr Val Arg Val Arg Asp Leu Asn Thr Val Tyr Gly Asp Asp
725 730 735

Tyr Asp Glu Ser Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp Asn
740 Cad 7 745 750

Ala Pro Val Trp Val Glu Gly Thr Leu Glu Gln Asn Phe Arg Val Arg
755 760 765

Glu Met Ser Ala Gly Gly Leu Val Val Gly Ser Val Arg Ala Asp Asp
770 775 780

Ile Asp Gly Pro Leu Tyr Asn Gln Val Arg Tyr Thr Ile Phe Pro Arg
785 790 795 800

Glu Asp Thr Asp Lys Asp Leu Ile Met Ile Asp Phe Leu Thr Gly Gln
805 810 815

Ile Ser Val Asn Thr Ser Gly Ala Ile Asp Ala Asp Thr Pro Pro Arg
820 825 830

Phe His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg Cys Ser Thr Glu
835 840 845

Asp Pro Ala Asp Cys Pro Pro Asp Pro Thr Tyr Trp Glu Thr Glu Gly
850 855 860

Asn Ile Thr Ile His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala
 865 Cad 8 870 875 880

Glu Thr Thr Lys Phe Asp Thr Val Val Tyr Ile Tyr Glu Asn Ala Thr
 885 890 895

His Leu Asp Glu Val Val Thr Leu Ile Ala Ser Asp Leu Asp Arg Asp
 900 905 910

Glu Ile Tyr His Thr Val Ser Tyr Val Ile Asn Tyr Ala Val Asn Pro
 915 920 925

Arg Leu Met Asn Phe Phe Ser Val Asn Arg Glu Thr Gly Leu Val Tyr
 930 935 940

Val Asp Tyr Glu Thr Gln Gly Ser Gly Glu Val Leu Asp Arg Asp Gly
 945 950 955 960

Asp Glu Pro Thr His Arg Ile Phe Phe Asn Leu Ile Asp Asn Phe Met
 965 970 975

Gly Glu Gly Glu Gly Asn Arg Asn Gln Asn Asp Thr Glu Val Leu Val
 980 985 990

Ile Leu Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Pro Pro Pro Ser
 995 1000 1005

Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln Gly Val Arg Leu
 1010 1015 1020

Glu Pro His Ile Phe Ala Pro Asp Arg Asp Glu Pro Asp Thr Asp Asn
 1025 1030 1035 1040

Ser Arg Val Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg Asp Ile
 1045 1050 1055

Glu Val Pro Glu Leu Phe Val Met Ile Gln Ile Ala Asn Val Thr Gly
 1060 1065 1070

Glu Leu Glu Thr Ala Met Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala
 1075 1080 1085

Ile His Ile Arg Ala Phe Asp His Gly Ile Pro Gln Met Ser Met Asn
 1090 1095 1100

Glu Thr Tyr Glu Leu Ile Ile His Pro Phe Asn Tyr Tyr Ala Pro Glu
 1105 Cad 10 1110 1115 1120

Phe Val Phe Pro Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg
 1125 1130 1135

Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly Glu Phe Leu Glu
 1140 1145 1150

Arg Ile Ser Ala Thr Asp Pro Asp Gly Leu His Ala Gly Val Val Thr
1155 1160 1165

Phe Gln Val Val Gly Asp Glu Glu Ser Gln Arg Tyr Phe Gln Val Val
1170 1175 1180

Asn Asp Gly Glu Asn Leu Gly Ser Leu Arg Leu Leu Gln Ala Val Pro
1185 1190 1195 1200

Glu Glu Ile Arg Glu Phe Arg Ile Thr Ile Arg Ala Thr Asp Gln Gly
1205 1210 1215

Thr Asp Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val Val Phe
1220 1225 *cad II* 1230

Val Pro Thr Gln Gly Glu Pro Arg Phe Ala Ser Ser Glu His Ala Val
1235 1240 1245

Ala Phe Ile Glu Lys Ser Ala Gly Met Glu Glu Ser His Gln Leu Pro
1250 1255 1260

Leu Ala Gln Asp Ile Lys Asn His Leu Cys Glu Asp Asp Cys His Ser
1265 1270 1275 1280

Ile Tyr Tyr Arg Ile Ile Asp Gly Asn Ser Glu Gly His Phe Gly Leu
1285 1290 1295

Asp Pro Val Arg Asn Arg Leu Phe Leu Lys Glu Leu Ile Arg Glu
1300 1305 1310

Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala Ser Asn Ser Pro Asp
1315 1320 1325

Gly Gly Ile Pro Leu Pro Ala Ser Ile Leu Thr Val Thr Val Thr Val
1330 1335 ██████████ 1340

Arg Glu Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr Thr Ala
1345 1350 1355 1360

Gly Ile Ser Thr Ala Asp Ser Ile Gly Arg Glu Leu Leu Arg Leu His
1365 1370 1375

Ala Thr Gln Ser Glu Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr Asp
1380 1385 1390

Thr Met Val Val Asp Pro Ser Leu Glu Ala Val Arg Gln Ser Ala Phe
1395 1400 1405

Val Leu Asn Ala Gln Thr Gly Val Leu Thr Leu Asn Ile Gln Pro Thr
1410 1415 1420

Ala Thr Met His Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr
1425 1430 1435 1440

Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val Tyr Val Val Ser Ser
1445 1450 1455

Gln Asn Arg Val Tyr Phe Val Phe Val Asn Thr Leu Gln Gln Val Glu
1460 1465 1470

Asp Asn Arg Asp Phe Ile Ala Asp Thr Phe Ser Ala Gly Phe Asn Met
1475 1480 1485

Thr Cys Asn Ile Asp Gln Val Val Pro Ala Asn Asp Pro Val Thr Gly
1490 1495 1500

Val Ala Leu Glu His Ser Thr Gln Met Ala Ala Thr Ser Tyr Gly Thr
1505 1510 1515 1520

Thr Tyr Pro Tyr Ser Leu Met Arg
1525

mp EC1
fat EC18
pc42 EC2
HPT-1 EC1
BTRcad-1
BTRcad-2
BTRcad-3
BTRcad-4
BTRcad-5
BTRcad-6
BTRcad-7
BTRcad-8
BTRcad-9
BTRcad-10
BTRcad-11

EWWMPPIFVYD
EDTVYSFDID
ASPVITLAI P
IVTENIWKAPKPV
ITANLGTVQVIYMDE
QNFEPCRVP
LEIIFAVQQFE
IHKERYLAIN
EHAQQTVTFD
RLPRGSPQVE
VEGTLEQNFRVR
ETTKFDTWVYIY
PPPSSELSWTIS
YFPPTNDAVIRLAR
ASSEHAVAF I

ENGK
ENAQR
ENTN
EMVEN
ITANLGTVQVIYMDE
ELGEP
EKSYQ
ETPL-TLNFDKEFG
ETRGE
NPVD
GLVVGSVR
DEVVTL I
NLKQ
GVRLEPHIF
GVLATVNGEFLERI
GMEESHQLPL

GPFPQRNLNQL
GYQVGGQT
GSLFP TPL
STPHPKITQ
PFLSGSYNLLMPVIRRVDN
FIELADGRISTEFMTFRIDS
VSIAADGRISTEFMTFRIDS
AIDGDTEINMPINYRLITNEEDTFFSIEALP66GS
FHDKDGLQNAQTYVRLESVDPPGAAEAFYIAPEV
AHDRD1GDDVVEHTLLGNAVNFLTIDKL
AIDDPDTADLRFEINWDTSFATKQGRQANPDEFRNCEIETIP
ADD1DGPLYNQVRYTIFPRETD1KD1LIMIELPH
ASDL1DRDEIYHMVSYVINYAVNPRLMNFFSVNRET
APDRDEPDTDNSRVGYEILNLSTERDIEVPELFVMIQIJIANVT
AQDIKNHLCEDDCHSIYYRI1DGNSEGHF

Cadherin Consensus Motif -----E-----G-----A.D.D.....

mp EC1
fat EC18
pc42 EC2
HPT-1 EC1
BTRcad-1
BTRcad-2
BTRcad-3
BTRcad-4
BTRcad-5
BTRcad-6
BTRcad-7
BTRcad-8
BTRcad-9
BTRcad-10
BTRcad-11

GWLILLHMP-
GMLTLTAR-
GN IYVTOP-
GSASSH-
GDEETFYIERTNIPNQWMWLNMТИGVNT
GAVFLV-
GYQRQTFIMGTLNHSIM-
GDIRVSANDSFN-
FPEINNINNRGLAIGRVVAREIRHNVT
GSNFRE-HKRRRIDANTPPRFHLYYTVA
BTRcad-4
BTRcad-5
BTRcad-6
BTRcad-7
BTRcad-8
BTRcad-9
BTRcad-10
BTRcad-11

DREK KIVKYELYGHAVSENGA-----
LDYEEVQHYILIVQAQDNNGQP-----
LDREERWDSYDLTIKVQDD66SP-----
IDREEKDAYFYAVAKDEYGK-----
HARQHYELPGMQQYMFNVRVD-----
SLNFVTSPLHFSVTALDSL-----
IDRDTLQREVFLPTIVAYKYDEE-----
IDYEVPEFQSITIRVVAATDNNDT-----
YHRESESELFVQVRATDTLGQP-----
IDYEEFEVSLTVRVRDLNTVY6-----
SDRCSTEDPACPDPT-----
IDNFMGEGEN-RNQNDTEVLVILLDMDNAPV
IDRDGDEPTHRIFFNLIDNFMGEGEN-RNQNDTEVLVILLDMDNAPV
GELETAMDLKGYMWGTYAIY1LAFDH6IPQMSSMNETYELIHPFNYYAPEF
EIREFRITIRATDQGTDP-----
GPLSTDMDTRVVVFVPTQGEPRF
LIRKDSASHTLQVAASNSPDGGI-----
GDPVRNRFLKKE-----

Cadherin Consensus Motif G.....

DRE.....
D.ND...P.F

F:3 2(6)

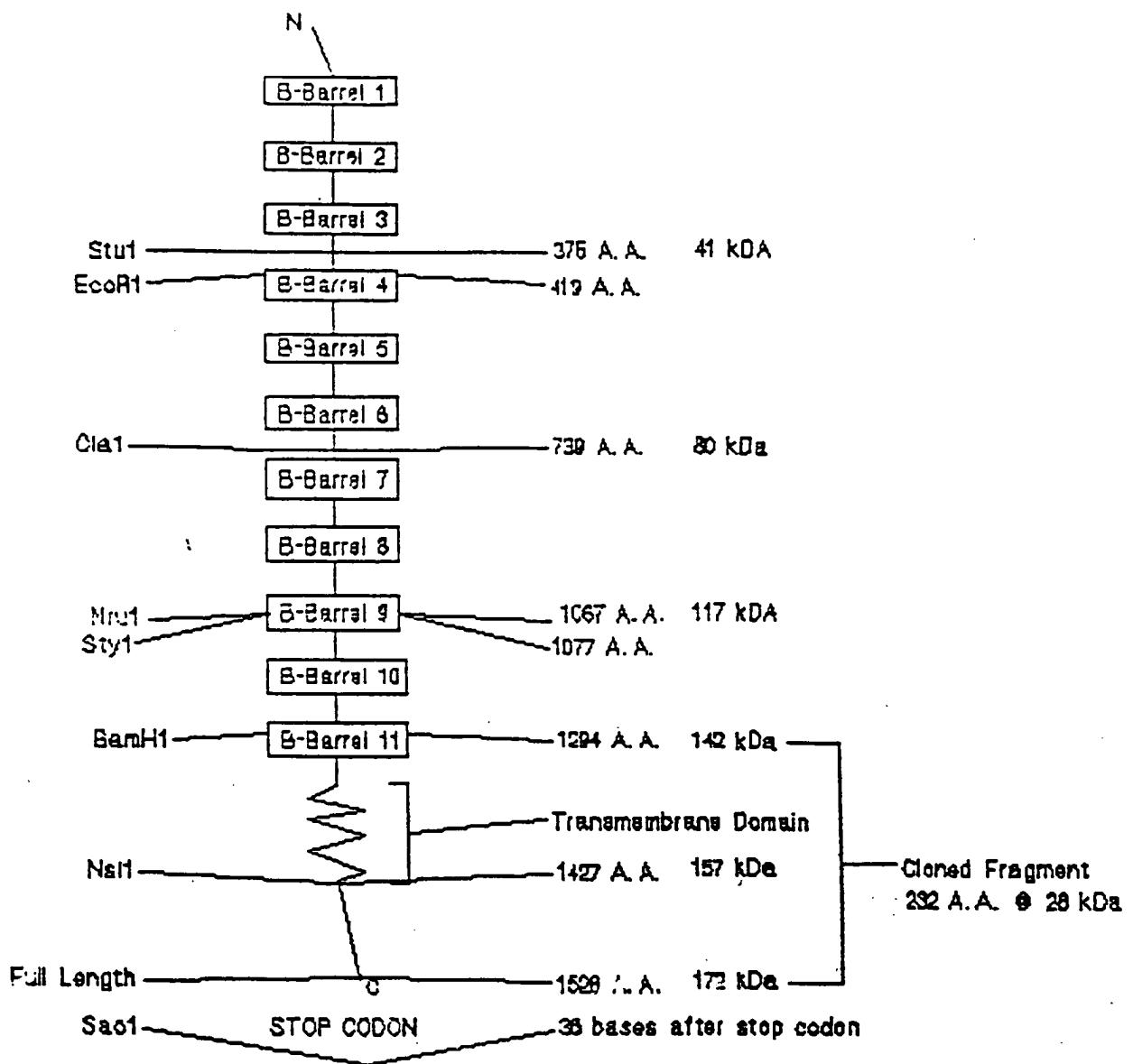


Fig. 3 Block diagram of cadherin-like structure of BT-R₁

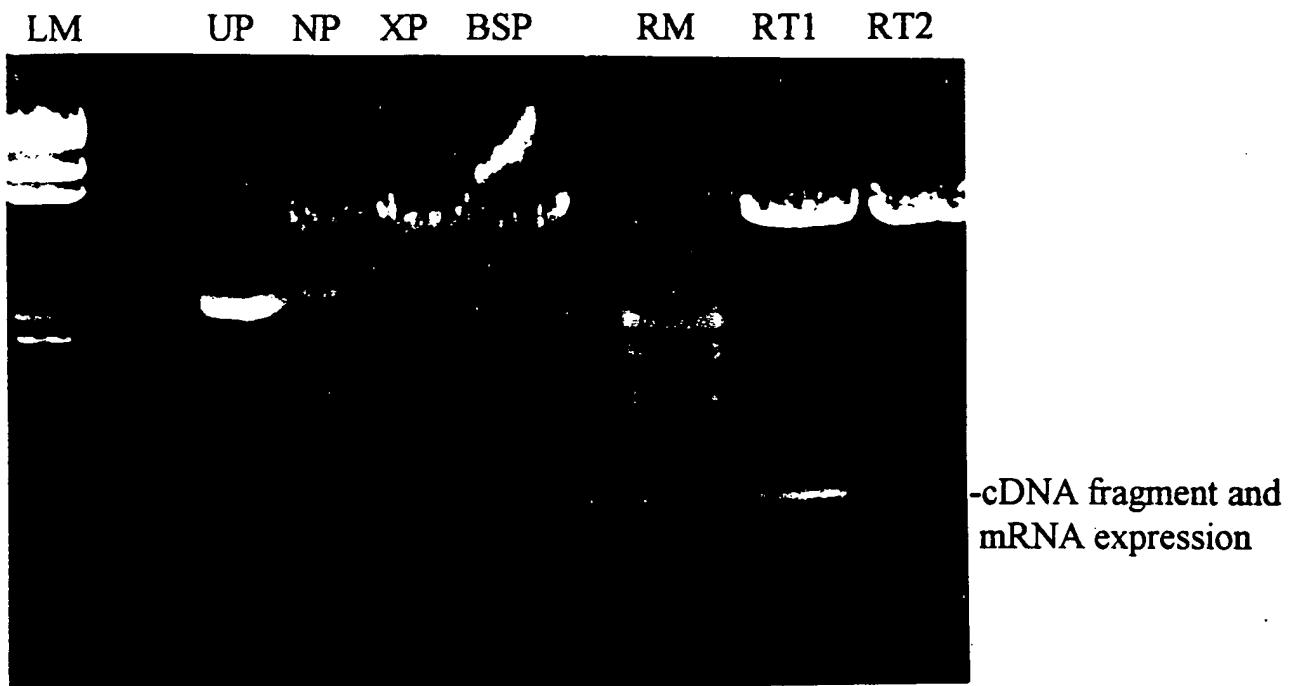


Fig. 7 Clone characterization of BamHI-SacI fragment of BT-R₁. LM is HindIII cut Lambda marker; UP is the uncut plasmid clone; NP is NsiI cut plasmid; XP is XhoI cut plasmid; BSP is BamHI and SacI cut plasmid showing the cloned fragment from BT-R₁; RM is mRNA size marker; and RT1 and RT2 are transcribed mRNAs from the cloned BT-R₁ fragment.

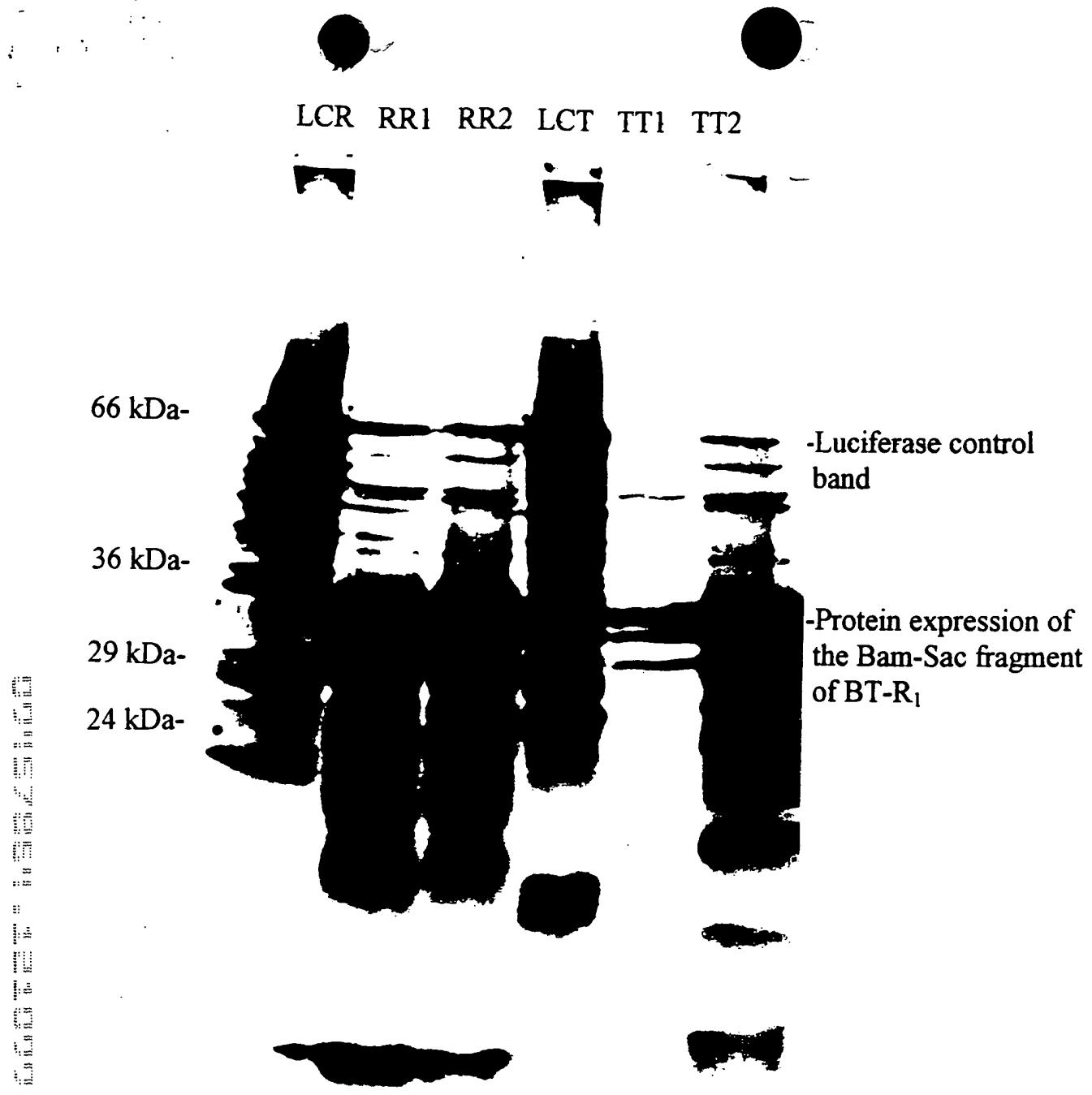


Fig. 5 Detection of protein expression from the plasmid containing the Bam-Sac fragment of BT-R₁ using ^{35}S -methionine as a tag. LCR is a luciferase control mRNA to show that the rabbit reticulocyte lysates are functional; RR1 and RR2 are expression products of the Bam-Sac fragment of BT-R₁ produced in rabbit reticulocytes from mRNA; LCT is a luciferase control plasmid to show that the transcription/translation kit is functional; and TT1 and TT2 are expression products of the Bam-Sac fragment of BT-R₁ produced in a transcription/translation kit.

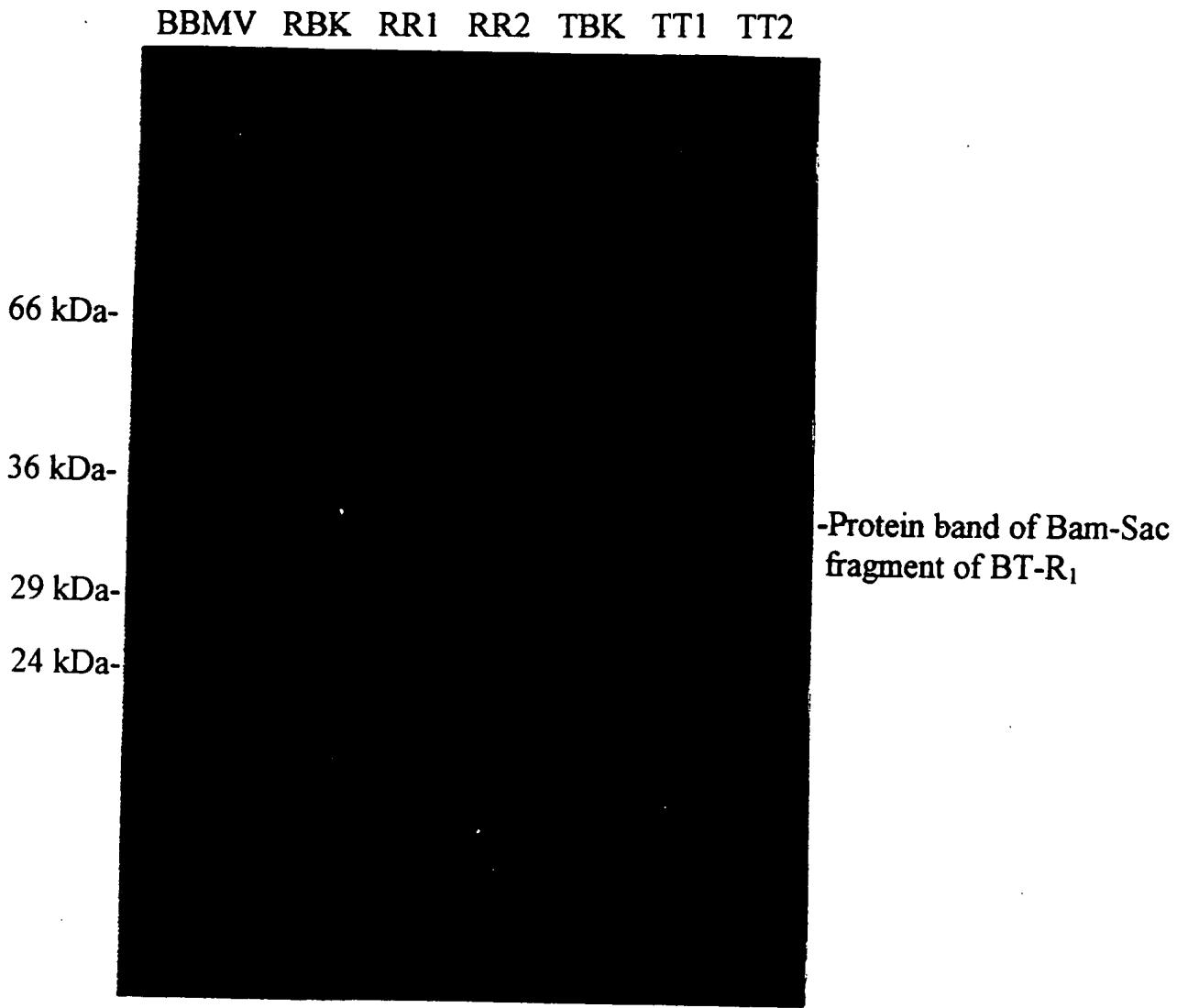
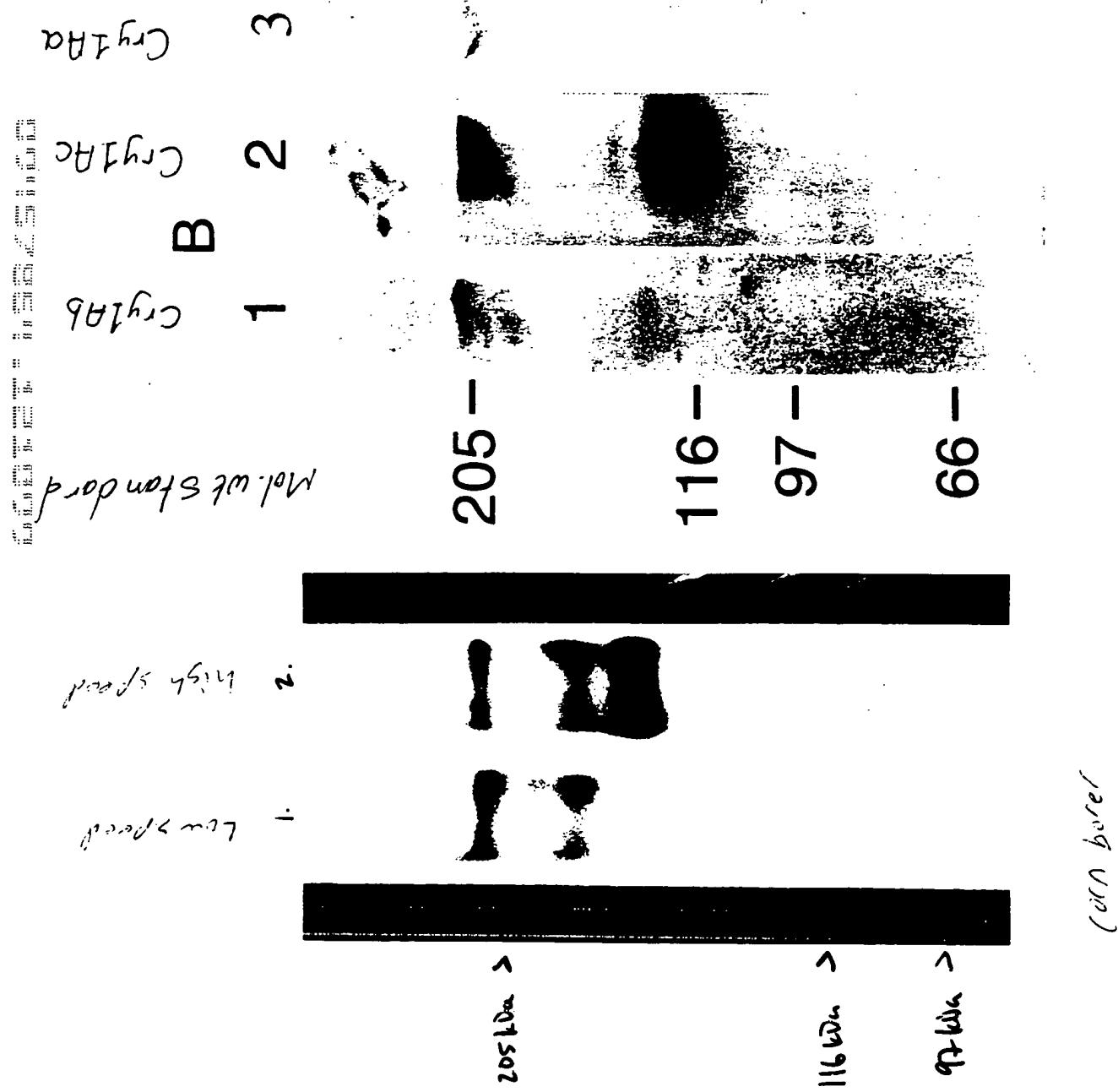


Fig. 6 Radio blot of the Bam-Sac fragment of BT-R₁ with ¹²⁵I-labeled Cry1Ab. BBMV is the brush border membrane vesicles from the midgut of *M. Sexta* containing the wild-type BT-R₁ receptor protein; RBK is a rabbit reticulocyte blank; RR1 and RR2 are the expression products of the Bam-Sac fragment of BT-R₁ produced in rabbit reticulocytes from mRNA; TBK is a transcription/translation kit blank; TT1 and TT2 are expression products of the Bam-Sac fragment of BT-R₁ produced in a transcription/translation kit. The arrows point to two of the bands.

BtMV proteins
(200ug) from the
Pink bollworm (*Gallerucida*
(*Pectinophora gossypiella*)
were separated by a
7.5% SDS-PAGE, blotted
and probed with 2×10^5 cpm
per ml of 125 I-labeled
Cry Toxins.

Fig 7



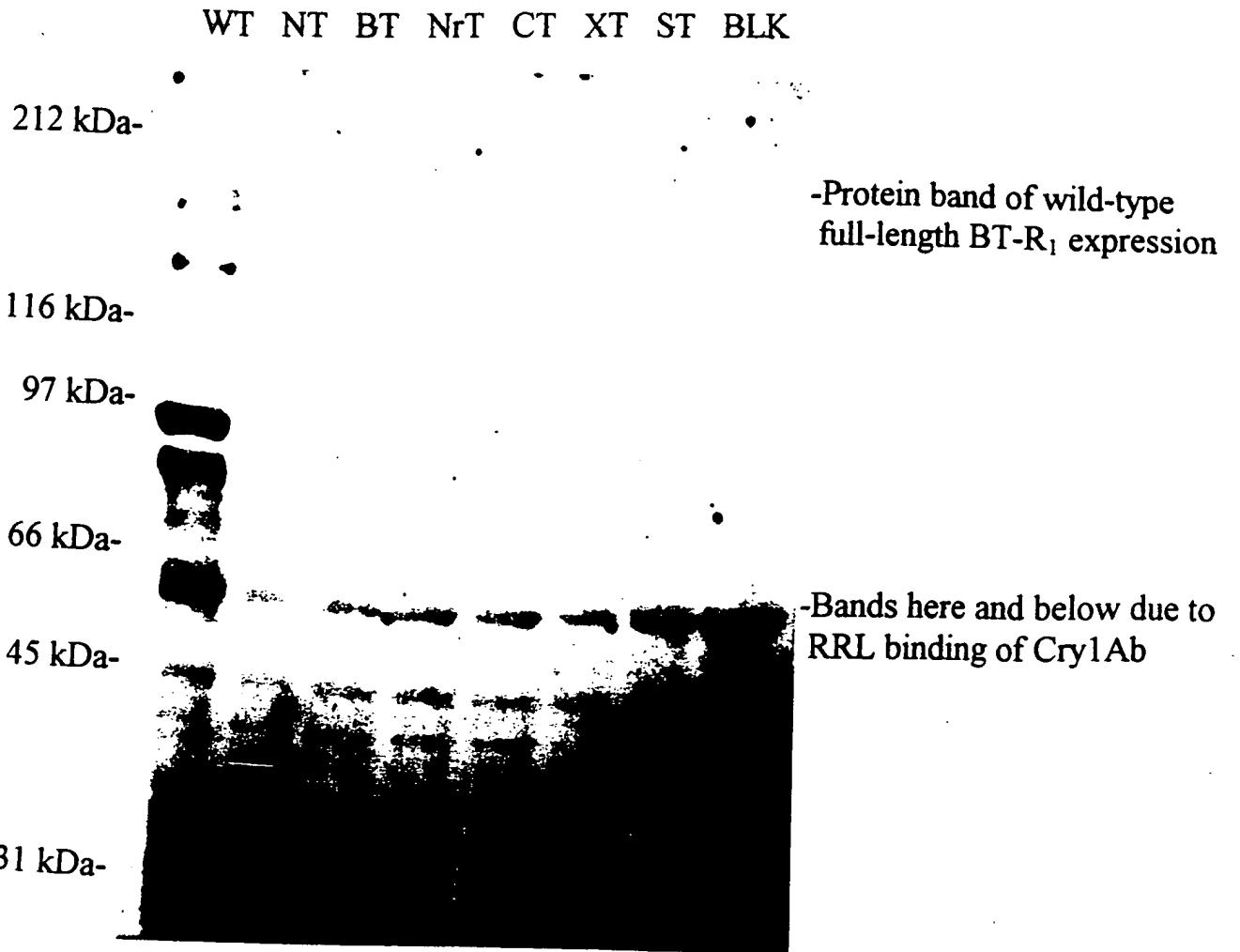


Fig. 8 Radio-blot of BT-R₁ and truncation mutants of BT-R₁ with ¹²⁵I-labeled Cry1Ab. WT is the wild-type full-length BT-R₁ receptor; NT is the truncation mutant resulting from NsiI digestion; BT is the mutant made with BamHI; NrT is the mutant made with NruI; CT is the mutant made with ClaI; XT is the mutant made with XhoI; ST is the mutant made with StuI; and, BLK is rabbit reticulocyte lysates containing only endogenous proteins.